In the Specification:

Please replace the paragraph beginning at page 15, line 9, with the following:

--The longer chain portion can be any of a variety of molecules which are inert to the subsequent conditions necessary for attaching the oligonucleotide probes, or for hybridization of a sample to the probe array. These longer chain portions will typically be ethylene glycol oligomers containing 2-14 monomer units, diamines, diacids, amino acids, peptides, or combinations thereof. In some embodiments, the longer chain portion is a polynucleotide (*e.g.,* a 15-mer of poly dT; SEQ ID NO:141). Additionally, for use in synthesis of the probe arrays, the linking group will typically have a protecting group, attached to a functional group (*i.e.,* hydroxyl, amino or carboxylic acid) on the distal or terminal end of the chain portion (opposite the solid support). After deprotection and coupling, the distal end is covalently bound to an oligonucleotide probe (*e.g.,* an HLA Class I oligonucleotide probe).--

Please replace the paragraph beginning at page 16, line 24, with the following:

--The length of the spacer between the support and the hybridization sequence influences the efficiency of hybridization (Guo et al, *Nuc. Acids Res.* **22**:5456-5465 (1994)). When large DNA fragments, such as PCR products, are allowed to hybridize with short oligonucleotide probes immobilized on solid supports, adequate distance between the hybridization sequence and the solid surface is required in order to achieve the efficient hybridization. This is due to the steric interference between large DNA molecules and the support. Within one embodiment of the invention, a 15-mer dT spacer (SEQ ID NO:141) was employed in each oligonucleotide probe to provide adequate space between hybridization sequence and the support. Although requiring extra expense in oligonucleotide synthesis, the 15-mer spacer was essential to optimize hybridization signals. Each completed probe contained a 5' amino group for

immobilization chemistry, a 20-nucleotide hybridization sequence, and a 15-mer dT spacer (SEQ ID NO:141) between them.--

Please replace the paragraph beginning at page 28, line 3, with the following:

--Once the solid support has been suitably derivatized, a linking group is attached to provide a spacing between the oligonucleotide probe and the support which is optimized for interactions between the probes and the sample. As provided above, a variety of linking groups can be used in this aspect of the invention. Preferred groups are those that provide a spacing similar to that provided by a 15-mer poly dT spacing group (SEQ ID NO:141). Additionally, the linking group will have a reactive portion that is selected to be compatible with the amino group of the aminoalkylsilane-derivatized support, or with the functional group present on the reagent used to facilitate linking group attachment (*e.g.*, the isothiocyanate portion of 1,4-phenylenediisothiocyanate). Accordingly, at the proximal end (that forming an attachment closest to the support), the linking group will have a functional group that is reactive with an amino moiety (*e.g.*, a carboxylic acid, anhydride, isothiocyanate, and the like) or a functional group that is reactive with an isocyanate, isothiocyanate or carboxylic acid moiety (*e.g.*, an amino group, a hydroxyl group or the like).--

Please replace the paragraph beginning at page 28, line 17, with the following:

--In a particularly preferred embodiment, the support is derivatized first with aminopropyltrimethoxysilane, followed by attachment of 1,4-phenylenediisothiocyanate, followed by attachment of a 15-mer oligonucleotide, preferably a 15-mer of poly-dT (SEQ ID NO:141).--

Please replace the paragraph beginning at page 37, line 1, with the following:

--Exon 2 of HLA-B gene was amplified by two-step asymmetric PCR. In the first step, the PCR primers were Exon 2 5'-primer (5'-GCTCCCACTCCATGAGGTAT-3'; SEQ ID NO:71) and Exon 2 3'-primer (5'-CGGCCTCGCTCTGGTTGTAG-3'; SEQ ID NO:138). The one hundred microliter amplification reaction contained 50 mM KCl, 10 mM Tris-HCl, 1.5 mg MgCl2, 10 mg of gelatin, 20 ng of genomic DNA, 2 microMoles of each primer, 200 microMoles each of dATP, dCTP, dTTP and dGTP, and 2.5 U of Taq DNA polymerase. The amplification reaction was performed in a Perkin-Elmer Cetus 9600 thermal cycler using 35 cycles of the following profile: 94°C for 30 seconds, 60°C for 1 minute and 72°C for 1 minute. The PCR mixture was then purified using a QIAGEN PCR purification kit (QIAGEN Inc., Chatsworth, CA) to remove the excess primers. In the second step, the PCR primer employed was a 5' Rhodamine-labeled Exon 2 3'-primer (SEQ ID NO:138). The PCR was performed in 30 cycles using the following profile: 94°C for 30 seconds, 60°C for 1 minute and 72°C for 2 minutes.--

Please replace the paragraph beginning at page 37, line 14, with the following:

--Amplification of exon 3 of HLA-B was accomplished using Exon 3 5'-primer (5'-ACCCGGTTTCATTTTCAGTTG-3'; SEQ ID NO:139) and Exon 3 3'-primer (5'-CCCACTGCCCCTGGTACC-3'; SEQ ID NO:140). The ampification reaction was performed in 35 cycles of the following profile: 94°C for 30 seconds, 65°C for 1 minute and 72°C for 1 minute. To generate single-strand exon 3 product, the second PCR was performed, employing a 5' Rhodamine-labeled 3 3'-primer (SEQ ID NO:140), in 30 cycles of the following profile: 94°C for 1 minute, 65°C for 1 minute and 72°C for 2 minutes.--